

bcRep news

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Changes in version 1.3.6 (2016-12-16)

BUG FIXES

- * `geneUsage()` & `compare.geneUsage()`: explained parameter 'abundance = "relative"' in help file
- * `compare.geneUsage()`: eliminated errors
- * `clones()`: eliminated error for 'useJ = FALSE'

NEW FEATURES AND FUNCTIONS

- * `clones.IDlist()`: returns a list containing the sequence ID's (from IMGT table) and the corresponding clone number

Changes in version 1.3.5 (2016-06-03)

BUG FIXES

- * `geneUsage.distance()`: eliminated errors
- * `geneUsage()` & `compare.geneUsage()`: eliminated errors

NEW FEATURES AND FUNCTIONS

- * `sequences.mutation.base()`: Added function to calculate proportions of silent mutations from nucleotide A to nucleotide B. Now, the nucleotide changes of the mutated position, but also the nucleotide distributions next to the mutated position (-3 to +3) can be analysed.
- * `plotSequencesMutationBase()`: added function to plot results of `sequences.mutation.base()`

Changes in version 1.3.4 (2016-04-21)

BUG FIXES

- * `clones()`: eliminated errors

Changes in version 1.3.3 (2016-04-15)

BUG FIXES

- * `clones.filterSize()`: eliminated errors
- * `clones.shared()`: eliminated errors
- * `clones.compareGeneUsage()`: eliminated errors

NEW FEATURES AND FUNCTIONS

- * `plotTrueDiversity()`: added option to plot mean diversities
- * `plotCompareTrueDiversity()`: added option to plot mean diversities

Changes in version 1.3.2 (2016-03-17)

BUG FIXES

- * `sequences.geneComb()`: eliminated errors
- * `compare.geneUsage()`: eliminated errors

Changes in version 1.3 (2016-02-25)

BUG FIXES

- * `readIMGT()`: eliminated errors
- * `clones()`: eliminated error message when no clone was found
- * `geneUsage()`: eliminated error for JH subgroup usage

NEW FEATURES AND FUNCTIONS

- * `sequences.mutation.AA()` added (proportions of amino acid mutations)
- * `plotSequencesMutationAA()` added
- * `sequences.mutation.base()` added (proportions of bases around mutations)
- * `plotSequencesMutationBase()` added

Changes in version 1.3 (2016-02-15)

BUG FIXES

- * `clones.shared()`: reduced computation time and memory; copy number of CDR3 sequences changed
- * `sequences.mutation()`: added sequence ID's

NEW FEATURES AND FUNCTIONS

- * added NEWS
- * `sequences.distance()` added (distance/dissimilarity measurements on sequence data)
- * `geneUsage.distance()` added (distance/dissimilarity measurements on gene usage data)
- * `dist.PCoA()` and `plotDistPCoA()` added (Principal coordinate analysis on distance data and visualization)

Changes in version 1.2.2 (2015-10-28)

BUG FIXES

- * `plotClonesCopyNumber()`: added parameter to plot with and without outliers (clone sizes > 75\% quantile)
- * `geneUsage()`: Combination of gene usage and functionality didn't work for alleles before
- * `sequences.geneComb()`: added parallel processing option

NEW FEATURES AND FUNCTIONS

- * added Vignette
- * `combineIMGT()`: combines IMGT output files from different folders
- * `clones.giniIndex()`: calculates Gini Index of clones
- * `clones.filterSize()`: filters clones for their size (number, percentage)
- * `clones.filterFuntionality()`: filters clones for their funtionality
- * `clones.filterJunctionFrame()`: filters clones for their junction frame usage
- * `compare.aaDistribution()`, `plotCompareAADistribution()`: compare amino acid distribution

of different samples
* `compare.trueDiversity()`, `plotCompareTrueDiversity()`: compare richness and diversity of different samples
* `compare.geneUsage()`, `plotCompareGeneUsage()`: compare gene usage of different samples (subgroup, gene, allele)

Version 1.0 (2015-10-09)